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NEWS	8	MAR 22	KOREAPAT now updated monthly; patent information enhanced
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NEWS	11	MAR 22	REGISTRY/ZREGISTRY enhanced with experimental property tags
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NEWS	16	APR 28	Improved searching of U.S. Patent Classifications for U.S. patent records in CA/CAplus
NEWS	17	MAY 23	GBFULL enhanced with patent drawing images
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NEWS	19	JUN 06	The Analysis Edition of STN Express with Discover! (Version 8.0 for Windows) now available
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NEWS	21	JUN 13	FRFULL enhanced with patent drawing images
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*ENCOMPLIT2    - EnCompass Literature File 1964-Present (Non-Supporters

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=> index bioscience
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                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       0.21       0.21

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
       AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS,
       BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB,
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74 FILES IN THE FILE LIST IN STNINDEX

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=> "(fluorescent resonance energy transfer"  or FRET) and histone and modification
UNMATCHED RIGHT PARENTHESIS 'FRET) AND'
The number of right parentheses in a query must be equal to the
number of left parentheses.

=> "(fluorescent resonance energy transfer" or FRET) and histone and modification
UNMATCHED RIGHT PARENTHESIS 'FRET) AND'
The number of right parentheses in a query must be equal to the
number of left parentheses.

=> ("fluorescent resonance energy transfer" or FRET) and histone and modification
          1    FILE BIOSIS
          1    FILE BIOTECHABS
          1    FILE BIOTECHDS
  17 FILES SEARCHED...
          1    FILE CAPLUS
          1    FILE CEABA-VTB
  29 FILES SEARCHED...
          2    FILE ESBIOBASE
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  46 FILES SEARCHED...
          1    FILE MEDLINE
  60 FILES SEARCHED...
          2    FILE SCISEARCH
        263    FILE USPATFULL
         21    FILE USPAT2
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  68 FILES SEARCHED...
         2   FILE WPIDS
         2   FILE WPINDEX

  14 FILES HAVE ONE OR MORE ANSWERS,   74 FILES SEARCHED IN STNINDEX

L1   QUE ("FLUORESCENT RESONANCE ENERGY TRANSFER" OR FRET) AND HISTONE AND MODI
       FICATION

=> d rank
F1          263   USPATFULL
F2           21   USPAT2
F3            2   ESBIOBASE
F4            2   IFIPAT
F5            2   SCISEARCH
F6            2   WPIDS
F7            2   WPINDEX
F8            1   BIOSIS
F9            1   BIOTECHABS
F10           1   BIOTECHDS
F11           1   CAPLUS
F12           1   CEABA-VTB
F13           1   FEDRIP
F14           1   MEDLINE


=> file esbiobase scisearch biosis biotechabs caplus
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                                                   ENTRY    SESSION
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=> ("fluorescent resonance energy transfer" or FRET) and histone and modification
L2            6 ("FLUORESCENT RESONANCE ENERGY TRANSFER" OR FRET) AND HISTONE
                AND MODIFICATION

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L3            6 DUP REMOVE L2 (0 DUPLICATES REMOVED)

=> d ti 1-6

L3   ANSWER 1 OF 6  SCISEARCH  COPYRIGHT (c) 2005 The Thomson Corporation  on
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TI   A fluorescence resonance energy transfer-based probe to monitor nucleosome
     structure

L3   ANSWER 2 OF 6  CAPLUS  COPYRIGHT 2005 ACS on STN
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TI Genetically encoded fusion protein fluorescent reporters of kinase, methyltransferase, and acetyltransferase activities in cells and tissues

L3 ANSWER 3 OF 6 Elsevier BIOBASE COPYRIGHT 2005 Elsevier Science B.V. on STN
TI A genetically encoded fluorescent reporter of **histone** phosphorylation in living cells

L3 ANSWER 4 OF 6 Elsevier BIOBASE COPYRIGHT 2005 Elsevier Science B.V. on STN
TI Modulation of DNA conformations through the formation of alternative high-order HU-DNA complexes

L3 ANSWER 5 OF 6 SCISEARCH COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Interaction of maize Opaque-2 and the transcriptional co-activators GCN5 and ADA2, in the modulation of transcriptional activity

L3 ANSWER 6 OF 6 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Selective recognition of acetylated **histones** by bromodomain proteins visualized in living cells.

=> d ab bib 1-6

L3 ANSWER 1 OF 6 SCISEARCH COPYRIGHT (c) 2005 The Thomson Corporation on STN
AB Nucleosomes are the basic units of eukaryotic chromatin structure. By restricting factor access to regulatory DNA sequences, nucleosomes significantly impact genomic processes such as transcription, and various mechanisms to alter nucleosome structure to relieve this repression have evolved. Both nucleosomes and processes that alter them are inherently dynamic in nature. Thus, studies of dynamics will be necessary to truly understand these relief mechanisms. We describe here the characteristics of a novel fluorescence resonance energy transfer-based reporter that can clearly signal the formation of a canonical nucleosome structure and follow conformational and compositional changes in that structure, both at the ensemble-average (bulk) and at the single molecule level. Labeled nucleosomes behave conformationally and thermodynamically like typical nucleosomes; thus they are relevant reporters of nucleosome behavior. Nucleosomes and free DNA are readily distinguishable at the single-molecule level. Thus, these labeled nucleosomes are well suited to studies of dynamic changes in nucleosome structure including single-molecule dynamics. © 2005 Elsevier Inc. All rights reserved.
AN 2005:525011 SCISEARCH
GA The Genuine Article (R) Number: 926KR
TI A fluorescence resonance energy transfer-based probe to monitor nucleosome structure
AU Lovullo D; Daniel D; Yodh J; Lohr D; Woodbury N W (Reprint)
CS Arizona State Univ, Dept Chem & Biochem, Tempe, AZ 85287 USA (Reprint); Midwestern Univ, Coll Osteopath Med, Div Basic Sci, Glendale, AZ 85308 USA; Arizona State Univ, Biodesign Inst, Tempe, AZ 85287 USA nwoodbury@asu.edu
CYA USA
SO ANALYTICAL BIOCHEMISTRY, (1 JUN 2005) Vol. 341, No. 1, pp. 165-172. ISSN: 0003-2697.
PB ACADEMIC PRESS INC ELSEVIER SCIENCE, 525 B ST, STE 1900, SAN DIEGO, CA 92101-4495 USA.
DT Article; Journal
LA English
REC Reference Count: 53
ED Entered STN: 2 Jun 2005
Last Updated on STN: 2 Jun 2005
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L3 ANSWER 2 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN

AB The invention provides fusion protein reporter mols. that can be used to monitor protein **modifications** (e.g., **histone modifications**) in living cells, and methods of using the fusion reporter mols. for diagnosing protein-**modification**-associated disorders (e.g. **histone-modification**-associated disorders). Reporters are designed by fusing, in order from N- to C-terminus, cyan fluorescent protein (CFP), a binding domain specific for the modified **histone** sequence of interest, a peptide substrate corresponding to the N-terminus of **histone** H3 or H4, and yellow fluorescent protein (YFP). **Modification** of the peptide substrate by a kinase, acetyltransferase, or methyltransferase then allows it to form an intramol. complex with the binding domain, increasing fluorescence resonance energy transfer (**FRET**) between the two flanking fluorescent moieties. Removal of the **modification** by a phosphatase, deacetylase, or (if methylation is reversible) demethylase reverses the **FRET** change. This design is optimized empirically to maximize responsivity by interchanging the donor and acceptor or the substrate and binding domain, or by varying the length and content of interdomain spacer sequences (linker sequences). Gcn5-based and TAFAB-based **histone** acetylation reporters are emphasized. The invention also provides methods of using the fusion protein reporters to identify candidate pharmaceutical agents that effect protein **modification** in cells and tissues, thus permitting identification of candidate pharmaceutical agents for treatment of protein-**modification**-associated disorders.

AN 2004:430935 CAPLUS

DN 141:18691

TI Genetically encoded fusion protein fluorescent reporters of kinase, methyltransferase, and acetyltransferase activities in cells and tissues

IN Ting, Alice Y.

PA Massachusetts Institute of Technology, USA

SO PCT Int. Appl., 96 pp.
CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2004044168	A2	20040527	WO 2003-US36059	20031112
	WO 2004044168	C1	20040722		
	WO 2004044168	A3	20041021		
	W: CA, JP				
	RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR				
	US 2004265906	A1	20041230	US 2003-634740	20030805
PRAI	US 2002-425578P	P	20021112		
	US 2003-634740	A	20030805		

L3 ANSWER 3 OF 6 Elsevier BIOBASE COPYRIGHT 2005 Elsevier Science B.V. on STN

AB An increase in **FRET** indicates phosphorylation of **histone** H3 at serine 28. The protein-based reporter (see picture) responds to phosphorylation through intramolecular complexation between a substrate domain derived from **histone** H3 and a linked phosphoserine-recognition domain. The reporter is also effective inside living mammalian cells. **FRET** = fluorescence resonance energy transfer.

AN 2004244172 ESBIOBASE

TI A genetically encoded fluorescent reporter of **histone** phosphorylation in living cells

AU Lin C.-W.; Ting A.Y.

CS Prof. A.Y. Ting, Department of Chemistry, Massachusetts Inst. of

Technology, Cambridge, MA 02139, United States.
E-mail: ating@mit.edu
SO Angewandte Chemie - International Edition, (24 MAY 2004), 43/22 (2940-2943), 15 reference(s)
CODEN: ACIEAY ISSN: 1433-7851
DT Journal; Article
CY Germany, Federal Republic of
LA English
SL English

L3 ANSWER 4 OF 6 Elsevier BIOBASE COPYRIGHT 2005 Elsevier Science B.V. on STN
AB HU is an abundant, highly conserved protein associated with the bacterial chromosome. It belongs to a small class of proteins that includes the eukaryotic proteins TBP, SRY, HMG-I and LEF-I, which bind to DNA non-specifically at the minor groove. HU plays important roles as an accessory architectural factor in a variety of bacterial cellular processes such as DNA compaction, replication, transposition, recombination and gene regulation. In an attempt to unravel the role this protein plays in shaping nucleoid structure, we have carried out fluorescence resonance energy transfer measurements of HU-DNA oligonucleotide complexes, both at the ensemble and single-pair levels. Our results provide direct experimental evidence for concerted DNA bending by HU, and the abrogation of this effect at HU to DNA ratios above about one HU dimer per 10-12 bp. These findings support a model in which a number of HU molecules form an ordered helical scaffold with DNA lying in the periphery. The abrogation of these nucleosome-like structures for high HU to DNA ratios suggests a unique role for HU in the dynamic modulation of bacterial nucleoid structure. .COPYRGT. 2004 Elsevier Ltd. All rights reserved.
AN 2004193691 ESBIOBASE
TI Modulation of DNA conformations through the formation of alternative high-order HU-DNA complexes
AU Sagi D.; Friedman N.; Vorgias C.; Oppenheim A.B.; Stavans J.
CS J. Stavans, Dept. of Physics of Complex Systems, The Weizmann Institute of Science, Rehovot, Israel.
E-mail: joel.stavans@weizmann.ac.il
SO Journal of Molecular Biology, (06 AUG 2004), 341/2 (419-428), 41 reference(s)
CODEN: JMOBAK ISSN: 0022-2836
PUI S0022283604006916
DT Journal; Article
CY United Kingdom
LA English
SL English

L3 ANSWER 5 OF 6 SCISEARCH COPYRIGHT (c) 2005 The Thomson Corporation on STN
AB Maize Opaque-2 (ZmO2), a bZip class transcription factor has been shown to activate the transcription of a series of genes expressed in the maturation phase of endosperm development. Activation requires the presence of one or more enhancer binding sites, which confer the propensity for activation by ZmO2 on heterologous promoters and in heterologous plant cell types, such as tobacco mesophyll protoplasts. The region of ZmO2 required for conferring transcriptional activation has been localised to a stretch of acidic residues in the N-terminal portion of the ZmO2 sequence, which is conserved between O2-related bZip factor sequences. Previously we identified the maize homologues of yeast transcriptional co-activators GCN5 and ADA2 that are implicated in nucleosome **modification** and transcription. In the present study we have shown that transcriptional modulation by ZmO2 involves the intranuclear interaction of ZmO2 with ZmADA2 and ZmGCN5. Forster resonance energy transfer (**FRET**) based techniques have enabled us to estimate the intracellular site of these intermolecular

interactions. As a functional readout of these intranuclear interactions, we used the ZmO2 responsive maize b-32 promoter to drive the beta-glucuronidase (GUS) in the presence and absence of ZmGCN5 and ZmADA2. Our results suggest that the likely recruitment of ZmADA2 and ZmGCN5 modulates the transactivation of b-32 promoter by ZmO2 and that there may be a competition between ZmGCN5 and ZmO2 for binding to the amino-terminal of ZmADA2. The results may be taken as a paradigm for other processes of transcriptional modulation in planta involving acidic activation domains.

AN 2005:19126 SCISEARCH
GA The Genuine Article (R) Number: 879AZ
TI Interaction of maize Opaque-2 and the transcriptional co-activators GCN5 and ADA2, in the modulation of transcriptional activity
AU Bhat R A; Borst J W; Riehl M; Thompson R D (Reprint)
CS INRA, Res Unit Genet & Ecophysiol Grain Legumes URLEG, BP 86510, F-21065 Dijon, France (Reprint); Max Planck Inst Plant Breeding Res, D-50829 Cologne, Germany; Univ Wageningen & Res Ctr, Microspectrometry Ctr, NL-6703 HA Wageningen, Netherlands
thompson@epoisses.inra.fr
CYA France; Germany; Netherlands
SO PLANT MOLECULAR BIOLOGY, (MAY 2004) Vol. 55, No. 2, pp. 239-252. ISSN: 0167-4412.
PB KLUWER ACADEMIC PUBL, VAN GODEWIJCKSTRAAT 30, 3311 GZ DORDRECHT, NETHERLANDS.
DT Article; Journal
LA English
REC Reference Count: 65
ED Entered STN: 13 Jan 2005
Last Updated on STN: 13 Jan 2005
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L3 ANSWER 6 OF 6 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
AB Acetylation and other **modifications** on **histones** comprise **histone** codes that govern transcriptional regulatory processes in chromatin. Yet little is known how different **histone** codes are translated and put into action. Using fluorescence resonance energy transfer, we show that bromodomain-containing proteins recognize different patterns of acetylated **histones** in intact nuclei of living cells. The bromodomain protein Brd2 selectively interacted with acetylated lysine 12 on **histone** H4, whereas TAFdblvert250 and PCAF recognized H3 and other acetylated **histones**, indicating fine specificity of **histone** recognition by different bromodomains. This hierarchy of interactions was also seen in direct peptide binding assays. Interaction with acetylated **histone** was essential for Brd2 to amplify transcription. Moreover association of Brd2, but not other bromodomain proteins, with acetylated chromatin persisted on chromosomes during mitosis. Thus the recognition of **histone** acetylation code by bromodomains is selective, is involved in transcription, and potentially conveys transcriptional memory across cell divisions.

AN 2004:149090 BIOSIS
DN PREV200400152814
TI Selective recognition of acetylated **histones** by bromodomain proteins visualized in living cells.
AU Kanno, Tomohiko; Kanno, Yuka; Siegel, Richard M.; Jang, Moon Kyoo; Lenardo, Michael J.; Ozato, Keiko [Reprint Author]
CS Laboratory of Molecular Growth Regulation, National Institute of Child Health and Human Development, National Institutes of Health, Bethesda, MD, 20892, USA
ozatok@nih.gov
SO Molecular Cell, (January 16 2004) Vol. 13, No. 1, pp. 33-43. print. ISSN: 1097-2765 (ISSN print).
DT Article
LA English
ED Entered STN: 17 Mar 2004